SEQUENCE LISTING

<110> Zonana et al.

<120> Hypohydrotic ectodermal dysplasia genes and proteins

<130> 55924

<140> 09/729,658
<141> 2000-12-04

<150> 09/342,681
<151> 1999-06-29

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<151> 1998-07-09

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<170> PatentIn Ver. 2.1

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c atg ggc tac ccg gag gtg gag cgc agg gaa ctc ctg cct gca gca gcg 289
Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
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ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc 337
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
20 25 30

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Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
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ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg 433
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
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tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc   529
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
                 85                  90                  95

gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag   577
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
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cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag   625
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
        115                 120                 125

gac ggg cac cag atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag   673
Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
    130                 135                 140

cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc   721
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160

aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga   769
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175

aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga   817
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190

cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att   865
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
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cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt   913
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225                 230                 235                 240

gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa   1009
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Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
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gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc   1105
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
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agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat   1201
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
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gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc   1249
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
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gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc   1297
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ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac   1345
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
        355                 360                 365

atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg   1393
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
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ctg ggt gaa gcc cct gca tcc tag attcccccat tttgcctctg tccgtgcccc  1447
Leu Gly Glu Ala Pro Ala Ser
385                 390

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Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
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Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
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Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
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Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
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Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
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Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
        195                 200                 205
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Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                245                 250                 255
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
            260                 265                 270
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285
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305                 310                 315                 320
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
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Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
            340                 345                 350
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
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tagtggttgt ctctggaggc c atg ggc tac cca gag gta gag cgc agg gaa 171
Met Gly Tyr Pro Glu Val Glu Arg Arg Glu
1 5 10

ccc ctg cct gcg gca gcg cca agg gag cgg ggc agc cag ggc tgc ggc 219
Pro Leu Pro Ala Ala Ala Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly

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tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gga acc   363
Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr
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gag tcc cgc ctc ggt ggc ccg ggt gct cct ggc acc tct ggc acc cta   411
Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu
 75                  80                  85                  90

agc agc cct ggg agc ctc gac ccg gtg ggt ccc atc acc cgc cac ctg   459
Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu
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ggg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca   507
Gly Gln Pro Ser Phe Gln Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro
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ctc ccc cct gag tcc cag gac cgg cac cag atg gcc ctc ctg aat ttc   555
Leu Pro Pro Glu Ser Gln Asp Arg His Gln Met Ala Leu Leu Asn Phe
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Phe Phe Pro Asp Glu Lys Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val
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155                 160                 165                 170

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Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile
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cca gga att cct ggg att cca gga aca act gtt atg gga cca cct ggc   795
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cca cct ggc cct cct ggt cct caa gga ccc cct ggc ctc caa gga cct   843
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    220                 225                 230

tct ggt gct gct gat aaa act gga act cgg gaa aat cag cca gct gtg   891
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235                 240                 245                 250
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tca ggt gga gtg ctc aat gac tgg tct cgc atc act atg aac cct aag   987
Ser Gly Gly Val Leu Asn Asp Trp Ser Arg Ile Thr Met Asn Pro Lys
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gtg ttt aaa cta cat ccc cgc agc ggg gag ctg gag gtc tac tac atc   1035
Val Phe Lys Leu His Pro Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile
        285                 290                 295

aac ttc act gac ttt gcc agc tac gag gtg gtg gtg gat gag aag ccc   1083
Asn Phe Thr Asp Phe Ala Ser Tyr Glu Val Val Val Asp Glu Lys Pro
    300                 305                 310

ttc ctg cag tgc acc cgc agc att gag aca ggg aag acc aac tac aac   1131
Phe Leu Gln Cys Thr Arg Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn
315                 320                 325                 330

act tgc tat act gca ggc gtg tgc ctc ctc aag gcc agg cag aaa atc   1179
Thr Cys Tyr Thr Ala Gly Val Cys Leu Leu Lys Ala Arg Gln Lys Ile
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gcc gtg aag atg gtg cac gct gac atc tct atc aat atg agc aag cac   1227
Ala Val Lys Met Val His Ala Asp Ile Ser Ile Asn Met Ser Lys His
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acc acc ttc ttc ggg gcc atc agg ctg ggc gaa gcc cct gca tcc tag   1275
Thr Thr Phe Phe Gly Ala Ile Arg Leu Gly Glu Ala Pro Ala Ser
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attctcccat tccatcctgg cccatgcccc tgccccaggt ttgggagcca ggactcccag 1335

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ttcttaggct ccctgctgac tggcttatgg tgactcctca acccttaggt ccctcatcag 1575

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65                  70                  75                  80
Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu Ser Ser Pro Gly Ser Leu
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Asp Pro Val Gly Pro Ile Thr Arg His Leu Gly Gln Pro Ser Phe Gln
            100                 105                 110
Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro Leu Pro Pro Glu Ser Gln
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Asp Arg His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
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145                 150                 155                 160
Lys Ser Gly Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
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Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
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Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
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Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
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Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285
Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala
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Ser Tyr Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg
305                 310                 315                 320
Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly
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Val Cys Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His
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gatgtacttg taatttttac agatggccct attgaatttc ttcttccctg atgaaaagcc 180
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ggtccctttt cttatagagt ttatctccta gaggaagaga gaacaaagaa acaagatatt 180
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gtgaaaaaga ccctcccaca ccctgccatc tgattccctc ctgcagggcc tcaggcccct 780
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tgctcgcctt ctccgtagac ccatcttctg ctgggaaaag ctaacctcat tcgggtacca 240

ggtgtacttc caagagatc atg gcc cac gtc ggg gac tgc aaa tgg atg tcc  292
                    Met Ala His Val Gly Asp Cys Lys Trp Met Ser
                      1               5                  10

tgg ctc cca gtg ctg gtg gtg tct ctg atg tgc tca gcc aag gcg gag   340
Trp Leu Pro Val Leu Val Val Ser Leu Met Cys Ser Ala Lys Ala Glu
             15                  20                  25

gac tcc aac tgt ggt gag aac gaa tac cac aac cag act acc ggg ctg   388
Asp Ser Asn Cys Gly Glu Asn Glu Tyr His Asn Gln Thr Thr Gly Leu
         30                  35                  40

tgc cag cag tgt cct cca tgc aga cca ggg gag gag ccc tac atg tcc   436
Cys Gln Gln Cys Pro Pro Cys Arg Pro Gly Glu Glu Pro Tyr Met Ser
     45                  50                  55

tgt gga tac ggc act aaa gac gac gac tat ggc tgt gtg ccc tgc cct   484
Cys Gly Tyr Gly Thr Lys Asp Asp Asp Tyr Gly Cys Val Pro Cys Pro
 60                  65                  70                  75

gca gag aag ttc tcc aaa gga ggt tat cag ata tgc agg cgc cac aaa   532
Ala Glu Lys Phe Ser Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys
                 80                  85                  90

gac tgt gag ggc ttc ttc cgg gcc act gtg ctg aca cca gga gac atg   580
Asp Cys Glu Gly Phe Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met
             95                 100                 105

gaa aac gac gct gag tgt ggc cca tgt ctc cct ggc tac tac atg ctg   628
Glu Asn Asp Ala Glu Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu
        110                 115                 120

gaa aac aga ccc agg aac atc tat ggc atg gtc tgc tac tcc tgt ctc   676
Glu Asn Arg Pro Arg Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu
    125                 130                 135

ttg gca cct ccc aac acc aag gaa tgt gtg gga gcc act tct ggg gtt   724
Leu Ala Pro Pro Asn Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Val
140                 145                 150                 155

tca gca cac tca tcc agc act tcc ggt ggc agc acc ttg tct ccc ttc   772
Ser Ala His Ser Ser Ser Thr Ser Gly Gly Ser Thr Leu Ser Pro Phe
                160                 165                 170

cag cat gct cac aaa gag ctc tca ggc caa gga cac ctg gcc acc gcc   820
Gln His Ala His Lys Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala
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                175                 180                 185

ctg att att gcc atg tct acg atc ttc atc atg gcc att gcc atc gtc   868
Leu Ile Ile Ala Met Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val
        190                 195                 200

ctc atc atc atg ttc tac atc atg aag act aag ccg tca gct cca gcc   916
Leu Ile Ile Met Phe Tyr Ile Met Lys Thr Lys Pro Ser Ala Pro Ala
    205                 210                 215

tgc tgt agc agt ccc cca gga aag agc gca gaa gcc cca gct aac aca   964
Cys Cys Ser Ser Pro Pro Gly Lys Ser Ala Glu Ala Pro Ala Asn Thr
220                 225                 230                 235

cac gag gag aaa aaa gag gcc cca gac agt gtg gtg acg ttc cct gag   1012
His Glu Glu Lys Lys Glu Ala Pro Asp Ser Val Val Thr Phe Pro Glu
                240                 245                 250

aat ggt gag ttc cag aag ctg aca gca aca ccc aca aag acc ccc aaa   1060
Asn Gly Glu Phe Gln Lys Leu Thr Ala Thr Pro Thr Lys Thr Pro Lys
            255                 260                 265

agt gag aat gat gcc tcc tct gag aac gag cag ttg cta agt cgc agt   1108
Ser Glu Asn Asp Ala Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser
        270                 275                 280

gtg gac agt gat gaa gag cca gcc ccg gac aag cag ggg tcc cca gag   1156
Val Asp Ser Asp Glu Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu
    285                 290                 295

cta tgt ctg ctg tcg cta gtt cac ctg gcc agg gag aag tct gtg acc   1204
Leu Cys Leu Leu Ser Leu Val His Leu Ala Arg Glu Lys Ser Val Thr
300                 305                 310                 315

agt aac aag tct gct ggg atc cag agc cgg agg aaa aag ata ctg gat   1252
Ser Asn Lys Ser Ala Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp
                320                 325                 330

gtg tat gcc aac gtg tgt ggt gtt gtt gaa ggt ctc agc ccc acc gag   1300
Val Tyr Ala Asn Val Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu
            335                 340                 345

ttg ccg ttt gac tgc ctt gag aag aca agc cga atg ctc agc tct aca   1348
Leu Pro Phe Asp Cys Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr
        350                 355                 360

tac aac tct gag aag gcg gtc gtg aaa aca tgg cgc cac ctt gcc gag   1396
Tyr Asn Ser Glu Lys Ala Val Val Lys Thr Trp Arg His Leu Ala Glu
    365                 370                 375

agc ttt gga ctg aag agg gat gag att ggg ggc atg act gat ggc atg   1444
Ser Phe Gly Leu Lys Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met
380                 385                 390                 395

cag ctc ttt gac cgc atc agc acc gcg ggc tac agc atc cca gag ctg   1492
Gln Leu Phe Asp Arg Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu
                400                 405                 410
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ctc aca aag ttg gtg cag atc gag cgg ctg gat gct gtg gag tcc ttg 1540
Leu Thr Lys Leu Val Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu
415 420 425

tgt gca gac ata ttg gag tgg gct ggg gtt gta cca cct gcc tcc cca 1588
Cys Ala Asp Ile Leu Glu Trp Ala Gly Val Val Pro Pro Ala Ser Pro
430 435 440

ccc cca gct gcg tcc tga agagttgtct tggactgtct tccctgggac 1636
Pro Pro Ala Ala Ser
445

cagctgggga tccaatgaag tcacgaccga cagctgtgag tgatgctatc agactgccaa 1696

aactcaaggc atttcctggt gggtcactgt attccttagg ctgccctaag tagttcattg 1756

agcactcaaa tgaaccaaac catgtgggaa ggacacaggt gaagaatctg atcctgtctt 1816

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ctaggcaaat gaagggatgc ttttttaaaa agtagcaaaa gttataaggg tgatagagtc 1936

tcaaggggtt gaaagtggga acatcctaat gaagaaaata acttcaaggt tttagtaaaa 1996

cggttacaaa gtacaggcat cccacatcct tcatggcctc agacagagca tggtttgctg 2056

gcatgcccta tggtttcaga ggtaactcga cctgtgtttg cagtcacaca ccatggtata 2116

agccttgcag tcactagtgg aagaactcac catgtgtcac tgacatacaa ggcgtgtgtc 2176

tgtccagtca caagtgtggg cagatctggc ctccagcacc actcgcagcc acagcagtta 2236

caatgtcagg cttgtcttgc ttcaaaggga cgtgcgtcct atctagagaa ggaaatggtg 2296

acttgctcag agtttgacca tgcctgattc ctgggtgagg ctcgagtgag ttcaggcaca 2356

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agggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3720

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<213> Mus musculus

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<221> CDS
<222> (1)..(1347)

<400> 13

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Met Ala His Val Gly Asp Cys Lys Trp Met Ser Trp Leu Pro Val Leu
  1               5                  10                  15

gtg gtg tct ctg atg tgc tca gcc aag gcg gag gac tcc aac tgt ggt   96
Val Val Ser Leu Met Cys Ser Ala Lys Ala Glu Asp Ser Asn Cys Gly
             20                  25                  30

gag aac gaa tac cac aac cag act acc ggg ctg tgc cag cag tgt cct  144
Glu Asn Glu Tyr His Asn Gln Thr Thr Gly Leu Cys Gln Gln Cys Pro
         35                  40                  45

cca tgc aga cca ggg gag gag ccc tac atg tcc tgt gga tac ggc act  192
Pro Cys Arg Pro Gly Glu Glu Pro Tyr Met Ser Cys Gly Tyr Gly Thr
     50                  55                  60

aaa gac gac gac tat ggc tgt gtg ccc tgc cct gca gag aag ttc tcc  240
Lys Asp Asp Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
 65                  70                  75                  80
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aaa gga ggt tat cag ata tgc agg cgc cac aaa gac tgt gag ggc ttc   288
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                 85                  90                  95

ttc cgg gcc act gtg ctg aca cca gga gac atg gaa aac gac gct gag   336
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110

tgt ggc cca tgt ctc cct ggc tac tac atg ctg gaa aac aga ccc agg   384
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115                 120                 125

aac atc tat ggc atg gtc tgc tac tcc tgt ctc ttg gca cct ccc aac   432
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
    130                 135                 140

acc aag gaa tgt gtg gga gcc act tct ggg gtt tca gca cac tca tcc   480
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Val Ser Ala His Ser Ser
145                 150                 155                 160

agc act tcc ggt ggc agc acc ttg tct ccc ttc cag cat gct cac aaa   528
Ser Thr Ser Gly Gly Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175

gag ctc tca ggc caa gga cac ctg gcc acc gcc ctg att att gcc atg   576
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190

tct acg atc ttc atc atg gcc att gcc atc gtc ctc atc atc atg ttc   624
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205

tac atc atg aag act aag ccg tca gct cca gcc tgc tgt agc agt ccc   672
Tyr Ile Met Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Ser Ser Pro
    210                 215                 220

cca gga aag agc gca gaa gcc cca gct aac aca cac gag gag aaa aaa   720
Pro Gly Lys Ser Ala Glu Ala Pro Ala Asn Thr His Glu Glu Lys Lys
225                 230                 235                 240

gag gcc cca gac agt gtg gtg acg ttc cct gag aat ggt gag ttc cag   768
Glu Ala Pro Asp Ser Val Val Thr Phe Pro Glu Asn Gly Glu Phe Gln
                245                 250                 255

aag ctg aca gca aca ccc aca aag acc ccc aaa agt gag aat gat gcc   816
Lys Leu Thr Ala Thr Pro Thr Lys Thr Pro Lys Ser Glu Asn Asp Ala
            260                 265                 270

tcc tct gag aac gag cag ttg cta agt cgc agt gtg gac agt gat gaa   864
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275                 280                 285

gag cca gcc ccg gac aag cag ggg tcc cca gag cta tgt ctg ctg tcg   912
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
    290                 295                 300

cta gtt cac ctg gcc agg gag aag tct gtg acc agt aac aag tct gct   960
```

```
Leu Val His Leu Ala Arg Glu Lys Ser Val Thr Ser Asn Lys Ser Ala
305                 310                 315                 320

ggg atc cag agc cgg agg aaa aag ata ctg gat gtg tat gcc aac gtg   1008
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                325                 330                 335

tgt ggt gtt gtt gaa ggt ctc agc ccc acc gag ttg ccg ttt gac tgc   1056
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340                 345                 350

ctt gag aag aca agc cga atg ctc agc tct aca tac aac tct gag aag   1104
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355                 360                 365

gcg gtc gtg aaa aca tgg cgc cac ctt gcc gag agc ttt gga ctg aag   1152
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
    370                 375                 380

agg gat gag att ggg ggc atg act gat ggc atg cag ctc ttt gac cgc   1200
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385                 390                 395                 400

atc agc acc gcg ggc tac agc atc cca gag ctg ctc aca aag ttg gtg   1248
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                405                 410                 415

cag atc gag cgg ctg gat gct gtg gag tcc ttg tgt gca gac ata ttg   1296
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
            420                 425                 430

gag tgg gct ggg gtt gta cca cct gcc tcc cca ccc cca gct gcg tcc   1344
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Pro Pro Pro Ala Ala Ser
        435                 440                 445

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<213> Homo sapiens

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<221> CDS
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<400> 14

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Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
  1               5                  10                  15

ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc    96
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
            20                  25                  30
```

```
cgg gcg ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc   144
Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
         35                  40                  45

ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg   192
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
     50                  55                  60

cgc tcg gag ttg cgg cgg gaa cgt gga gcc gag tcc cgc ctt ggc ggc   240
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
 65                  70                  75                  80

tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc   288
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
                 85                  90                  95

gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag   336
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
            100                 105                 110

cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag   384
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
        115                 120                 125

gac ggg cac cag atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag   432
Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
    130                 135                 140

cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc   480
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160

aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga   528
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175

aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga   576
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190

cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att   624
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
        195                 200                 205

cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt   672
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
    210                 215                 220

cct caa gga ccc cct ggc ctc cag gga cct tct ggt gct gct gat aaa   720
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240

gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa   768
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                245                 250                 255

ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat   816
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Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
            260                 265                 270

gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc   864
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285

cgc agc ggg gag ctg gag gta ctg gtg gac ggc acc tac ttc atc tat   912
Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
    290                 295                 300

agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat   960
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305                 310                 315                 320

gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc   1008
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
                325                 330                 335

gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc   1056
Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
            340                 345                 350

ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac   1104
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
        355                 360                 365

atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg   1152
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
    370                 375                 380

ctg ggt gaa gcc cct gca tcc tag                                  1176
Leu Gly Glu Ala Pro Ala Ser
385                 390
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Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Pro Leu Pro Ala Ala Ala
  1               5                  10                  15

cca agg gag cgg ggc agc cag ggc tgc ggc tgt cgc ggg gcc cct gct    96
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Arg Gly Ala Pro Ala
            20                  25                  30

cgg gcg ggc gaa ggg aac agc tgc cgg ctc ttc ctg ggt ttc ttt ggc   144
Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu Phe Leu Gly Phe Phe Gly
        35                  40                  45
```

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ctc tcg ctg gcc ctc cac ctg ctg acg ctg tgc tgc tac cta gag ttg   192
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
     50                  55                  60

cgg tcc gaa ttg cgg cgg gaa cgg gga acc gag tcc cgc ctc ggt ggc   240
Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr Glu Ser Arg Leu Gly Gly
 65                  70                  75                  80

ccg ggt gct cct ggc acc tct ggc acc cta agc agc cct ggg agc ctc   288
Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu Ser Ser Pro Gly Ser Leu
                 85                  90                  95

gac ccg gtg ggt ccc atc acc cgc cac ctg ggg cag ccg tcc ttt caa   336
Asp Pro Val Gly Pro Ile Thr Arg His Leu Gly Gln Pro Ser Phe Gln
            100                 105                 110

cag cag cct ttg gaa ccg gga gaa gat cca ctc ccc cct gag tcc cag   384
Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro Leu Pro Pro Glu Ser Gln
        115                 120                 125

gac cgg cac cag atg gcc ctc ctg aat ttc ttc ttt cct gat gaa aag   432
Asp Arg His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
    130                 135                 140

gca tat tct gaa gag gaa agt agg cgt gtt cgc cgc aat aag aga agc   480
Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145                 150                 155                 160

aaa agt ggt gaa gga gca gat ggt cct gtt aaa aac aag aaa aag gga   528
Lys Ser Gly Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
                165                 170                 175

aag aag gca ggg cca cct ggg ccc aac ggc ccc cca gga cct cca gga   576
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
            180                 185                 190

cct ccg gga ccc cag gga cct cca ggg att cca gga att cct ggg att   624
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
        195                 200                 205

cca gga aca act gtt atg gga cca cct ggc cca cct ggc cct cct ggt   672
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
    210                 215                 220

cct caa gga ccc cct ggc ctc caa gga cct tct ggt gct gct gat aaa   720
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225                 230                 235                 240

act gga act cgg gaa aat cag cca gct gtg gtg cat ctg cag ggc caa   768
Thr Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
                245                 250                 255

ggg tca gca att caa gtc aaa aat gat ctt tca ggt gga gtg ctc aat   816
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
            260                 265                 270
```

```
gac tgg tct cgc atc act atg aac cct aag gtg ttt aaa cta cat ccc   864
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
        275                 280                 285

cgc agc ggg gag ctg gag gtc tac tac atc aac ttc act gac ttt gcc   912
Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala
    290                 295                 300

agc tac gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc acc cgc   960
Ser Tyr Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg
305                 310                 315                 320

agc att gag aca ggg aag acc aac tac aac act tgc tat act gca ggc   1008
Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly
                325                 330                 335

gtg tgc ctc ctc aag gcc agg cag aaa atc gcc gtg aag atg gtg cac   1056
Val Cys Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His
            340                 345                 350

gct gac atc tct atc aat atg agc aag cac acc acc ttc ttc ggg gcc   1104
Ala Asp Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala
        355                 360                 365

atc agg ctg ggc gaa gcc cct gca tcc tag                          1134
Ile Arg Leu Gly Glu Ala Pro Ala Ser
    370                 375
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<210> 16
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1347)

<400> 16

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atg gcc cat gtg ggg gac tgc acg cag acg ccc tgg ctc ccc gtc ctg   48
Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
  1               5                  10                  15

gtg gtg tct ctg atg tgc tca gcc cga gcg gaa tac tca aac tgc ggt   96
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
            20                  25                  30

gag aac gag tac tac aac cag act acg ggg ctg tgc cag gag tgc ccc   144
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
        35                  40                  45

ccg tgt ggg ccg gga gag gag ccc tac ctg tcc tgt ggc tac ggc acc   192
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
    50                  55                  60

aaa gac gag gac tac ggc tgc gtc ccc tgc ccg gcg gag aag ttt tcc   240
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
```

```
65                  70                  75                  80

aaa gga ggc tac cag ata tgc agg cgt cac aaa gac tgt gag ggc ttc   288
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                85                  90                  95

ttc cgg gcc acc gtg ctg aca cca ggg gac atg gag aat gac gct gag   336
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110

tgt ggc cct tgc ctc cct ggc tac tac atg ctg gag aac aga ccg agg   384
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115                 120                 125

aac atc tat ggc atg gtc tgc tac tcc tgc ctc ctg gca ccc ccc aac   432
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
    130                 135                 140

acc aag gaa tgt gtg gga gcc act tca gga gct tct gcc aac ttc cct   480
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145                 150                 155                 160

ggc acc tcg ggc agc agc acc ctg tct ccc ttc cag cac gcc cac aaa   528
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175

gaa ctc tca ggc caa gga cac ctg gcc act gcc ctg atc att gca atg   576
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190

tcc acc atc ttc atc atg gcc atc gcc atc gtc ctc atc atc atg ttc   624
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205

tac atc ctg aag aca aag ccc tct gcc cca gcc tgt tgc acc agc cac   672
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
    210                 215                 220

ccg ggg aag agc gtg gag gcc caa gtg agc aag gac gag gag aag aaa   720
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225                 230                 235                 240

gag gcc cca gac aac gtg gtg atg ttc tcc gag aag gat gaa ttt gag   768
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                245                 250                 255

aag ctg aca gca act cca gca aag ccc acc aag agc gag aac gat gcc   816
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
            260                 265                 270

tca tcc gag aat gag cag ctg ctg agc cgg agc gtc gac agt gat gag   864
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275                 280                 285

gag ccc gcc cct gac aag cag ggc tcc ccg gag ctg tgc ctg ctg tcg   912
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
    290                 295                 300
```

```
ctg gtt cac ctg gcc agg gag aag tct gcc acc agc aac aag tca gcc   960
Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
305                 310                 315                 320

ggg att caa agc cgg agg aaa aag atc ctc gat gtg tat gcc aac gtg   1008
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                325                 330                 335

tgt gga gtc gtg gaa ggt ctt agc ccc acg gag ctg cca ttt gat tgc   1056
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340                 345                 350

ctc gag aag act agc cga atg ctc agc tcc acg tac aac tct gag aag   1104
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355                 360                 365

gct gtt gtg aaa acg tgg cgc cac ctc gcc gag agc ttc ggc ctg aag   1152
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
    370                 375                 380

agg gat gag att ggg ggc atg aca gac ggc atg caa ctc ttt gac cgc   1200
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385                 390                 395                 400

atc agc acg gca ggc tac agc atc cct gag cta ctc aca aaa ctg gtg   1248
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                405                 410                 415

cag att gag cgg ctg gat gct gtg gag tcc ttg tgt gca gac ata ctg   1296
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
            420                 425                 430

gag tgg gcg ggg gtt gtg cca cct gcc tcc cag cca cat gct gca tcc   1344
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser
        435                 440                 445

tga                                                               1347
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<210> 17
<211> 448
<212> PRT
<213> Homo sapiens

<400> 17

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Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
  1               5                  10                  15
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
             20                  25                  30
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
         35                  40                  45
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
     50                  55                  60
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
 65                  70                  75                  80
```

```
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                 85                  90                  95
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115                 120                 125
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
    130                 135                 140
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145                 150                 155                 160
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
    210                 215                 220
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225                 230                 235                 240
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                245                 250                 255
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
            260                 265                 270
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275                 280                 285
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
    290                 295                 300
Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
305                 310                 315                 320
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                325                 330                 335
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340                 345                 350
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355                 360                 365
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
    370                 375                 380
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385                 390                 395                 400
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                405                 410                 415
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
            420                 425                 430
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser
        435                 440                 445
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<210> 18
<211> 4235
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (433)..(1779)

<400> 18
gggggcagac ggccgaagag ccaggtgtgc cagggaccta tggcagcagg gctgaacgtg 60

cccgctccag cctctccagt gctgggagag acctctagat ggtgcaggtg agtttgcaat 120

gagggaaagc ccctcggcaa ggactgagtt tccaaacttg cagacagggc agggagcggt 180

caaggaagag ttcccgggaa gccctttaaa cggaaaggaa gcggggctag tgtcagagag 240

gtgtgccagg tcccaggcag ccctgctgac ccctaaggac atagagtacc tgcttctgag 300

agggctgcca cggtggccac ctgtgaagcc tgtcacccag aactggatgg tacctgactt 360

tcttcataga cccatcttct gctgggactg aagctgacct ccaacagaag ccaggtgagc 420

ccttgggaga gg atg gcc cat gtg ggg gac tgc acg cag acg ccc tgg ctc 471
Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu
1 5 10

ccc gtc ctg gtg gtg tct ctg atg tgc tca gcc cga gcg gaa tac tca 519
Pro Val Leu Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser
15 20 25

aac tgc ggt gag aac gag tac tac aac cag act acg ggg ctg tgc cag 567
Asn Cys Gly Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln
30 35 40 45

gag tgc ccc ccg tgt ggg ccg gga gag gag ccc tac ctg tcc tgt ggc 615
Glu Cys Pro Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly
50 55 60

tac ggc acc aaa gac gag gac tac ggc tgc gtc ccc tgc ccg gcg gag 663
Tyr Gly Thr Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu
65 70 75

aag ttt tcc aaa gga ggc tac cag ata tgc agg cgt cac aaa gac tgt 711
Lys Phe Ser Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys
80 85 90

gag ggc ttc ttc cgg gcc acc gtg ctg aca cca ggg gac atg gag aat 759
Glu Gly Phe Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn
95 100 105

gac gct gag tgt ggc cct tgc ctc cct ggc tac tac atg ctg gag aac 807
Asp Ala Glu Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn
110 115 120 125

aga ccg agg aac atc tat ggc atg gtc tgc tac tcc tgc ctc ctg gca 855
Arg Pro Arg Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala
130 135 140

ccc ccc aac acc aag gaa tgt gtg gga gcc act tca gga gct tct gcc 903
Pro Pro Asn Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala
145 150 155

aac ttc cct ggc acc tcg ggc agc agc acc ctg tct ccc ttc cag cac 951

```
Asn Phe Pro Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His
        160                 165                 170

gcc cac aaa gaa ctc tca ggc caa gga cac ctg gcc act gcc ctg atc   999
Ala His Lys Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile
    175                 180                 185

att gca atg tcc acc atc ttc atc atg gcc atc gcc atc gtc ctc atc  1047
Ile Ala Met Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile
190                 195                 200                 205

atc atg ttc tac atc ctg aag aca aag ccc tct gcc cca gcc tgt tgc  1095
Ile Met Phe Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys
                210                 215                 220

acc agc cac ccg ggg aag agc gtg gag gcc caa gtg agc aag gac gag  1143
Thr Ser His Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu
            225                 230                 235

gag aag aaa gag gcc cca gac aac gtg gtg atg ttc tcc gag aag gat  1191
Glu Lys Lys Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp
        240                 245                 250

gaa ttt gag aag ctg aca gca act cca gca aag ccc acc aag agc gag  1239
Glu Phe Glu Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu
    255                 260                 265

aac gat gcc tca tcc gag aat gag cag ctg ctg agc cgg agc gtc gac  1287
Asn Asp Ala Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp
270                 275                 280                 285

agt gat gag gag ccc gcc cct gac aag cag ggc tcc ccg gag ctg tgc  1335
Ser Asp Glu Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys
                290                 295                 300

ctg ctg tcg ctg gtt cac ctg gcc agg gag aag tct gcc acc agc aac  1383
Leu Leu Ser Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn
            305                 310                 315

aag tca gcc ggg att caa agc cgg agg aaa aag atc ctc gat gtg tat  1431
Lys Ser Ala Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr
        320                 325                 330

gcc aac gtg tgt gga gtc gtg gaa ggt ctt agc ccc acg gag ctg cca  1479
Ala Asn Val Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro
    335                 340                 345

ttt gat tgc ctc gag aag act agc cga atg ctc agc tcc acg tac aac  1527
Phe Asp Cys Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn
350                 355                 360                 365

tct gag aag gct gtt gtg aaa acg tgg cgc cac ctc gcc gag agc ttc  1575
Ser Glu Lys Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe
                370                 375                 380

ggc ctg aag agg gat gag att ggg ggc atg aca gac ggc atg caa ctc  1623
Gly Leu Lys Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu
```

385 390 395

ttt gac cgc atc agc acg gca ggc tac agc atc cct gag cta ctc aca 1671
Phe Asp Arg Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr
400 405 410

aaa ctg gtg cag att gag cgg ctg gat gct gtg gag tcc ttg tgt gca 1719
Lys Leu Val Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala
415 420 425

gac ata ctg gag tgg gcg ggg gtt gtg cca cct gcc tcc cag cca cat 1767
Asp Ile Leu Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His
430 435 440 445

gct gca tcc tga aaagcatgcc tgtgggctgt cctcccagga caagccaagg 1819
Ala Ala Ser

atccaacgag ggctctggag ctgtgagtgg tgccaaaaga ctgccaagaa tcaaggcttt 1879

tgtgatatgt caccgtatgc cttaggatgt tcaaggagcc agacgaaata aggcctgtct 1939

tccaatttaa ccaaagataa aggactagag ccgggatact ttcagatgct cgcctgtacc 1999

tcaccaggca gagtaaatat ctactcactc atacagccag cccaccagcc caccattaac 2059

tcactgaaca atgagacaat gttgaggact caaatgaatc aaaccccgtg ggaatgacag 2119

aagtgaagaa tctggtccct gtctttaagg agtttgcact ccagtagaag acagaaggaa 2179

cgtatgttta caaaccactt cactggaaga cgtcaaacaa gctgaatgaa ggggcgctta 2239

gaaaacgtta atagaagttc taagcgggag atgactccct actgggatga tgaaggatgg 2299

catcctagtg aagaagcagc tcaaacattt tgataaaatg gcaacaaaat gcagacaccc 2359

tgctccaggt attatttcag gtttagtaca agtctgttaa taccctatgt ggtttcatta 2419

ggataacttt ttacctatcc ttgaggtcat ccatattctt acaggccttc cagtcaataa 2479

tggaagagct cactctatac aaaaccaata tgcaaggcat gtgtttgtcc aagcaattgg 2539

atgtgtgcag tagccaattt catttactgc attactcttt ggcctgggaa ccctgtggtc 2599

tgcactacat gtgaatggcc ttccacttca gtcttaggca gatttgacct tttaggggca 2659

gcaatgctga aggacacagc aatttaaatt ataatgtgtc aggctgtgtt ttcacttcaa 2719

acatgtatga gtagtcagct gtaattagag aaatgatgac ttcctaagag ttcagccacg 2779

cataattcta gatttcaaga gcatctaaga cttgtggatt agcctcatgg catgagagtt 2839

tcagactcag ccttctgagc cagtcaggga aagtggagtt ctgcagcgca aatgagagcc 2899

tgggcttggt gtcgagggag ctggcttcta gttgtgccac cttgggcctt gtcttttcct 2959

ctctctgcct cagtttctcg tctgccaatg agatgttagt tagtgattct ataattgggg 3019

caggtagggt tcaggtgagc aaaaagaaag tggagctata ggaaatgcca ggcctttgag 3079

gtgctctatg gaagtcaaca cagtgtggtt tgtccattta aatgggaata aaaacagaaa 3139

aactcagact tggcattttc acaataactg caatggtttg acataacatt tataggcaga 3199

aagttaataa actggcattg ttcttggcat attattgtac tatccctgta actgccaaga 3259

gctcaggagc caggctagtg atcacaccag gggttagagt tcactgctga actccctgat 3319

ggcaggtctg tgtttattac tacattaaaa caaagtctct gacttataaa gcgaggtcgt 3379

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acaccaacaa gcaatttccc accaacgaat gtagtacata ctgtgagagg atcataatga 3499

ggtcctgaat atttaatatc atcatttact gtgtctgttt gctgctgttt ttcgaaccta 3559

tttggtttac cctgcaagct aaatactcca cggcagagct taattatcct tttaattcct 3619

ctttgaaatc ctgtggtgcc cccttccccc tgccttgtga tgatgatgag tgagtctccc 3679

cttaattaga ctgcaaatgt cacttgtgat gagtgtgcca ttccaggata acagcttgca 3739

ccctcctcag aatgttttca gcgaaagagt ggggtggctg ttctctgctc ctggtgcttt 3799

ggcctcattt cacactatta gaattctggg gctgtaaggc cagccagtgt cagctcatgt 3859

tccattggct ctccacctgc catttttagg gagctattcc ttatatagtt acaaattccc 3919

ttgtcattta cttatttgga aacatgggat ttactctgac aagctttagc ctatgttatg 3979

ggattcagaa caatgagatc ataataattc tcactgacca aagctgggac tccatcctgc 4039

cattttgtg tggagatatt cataattctg caatacttta aaacatttag aaaacacccc 4099

agggtaggtc tgtggccctt agacagtgaa gtcttaattg tcaatattat ttttgtctaa 4159

ttctgtatat atataactta ttatatttta taatctcaat aaacacatta ataaaaaaaa 4219

aaaaaaaaaa aaaaaa 4235

<210> 19
<211> 448
<212> PRT
<213> Homo sapiens

<400> 19

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Met Ala His Val Gly Asp Cys Thr Gln Thr Pro Trp Leu Pro Val Leu
  1               5                  10                  15
Val Val Ser Leu Met Cys Ser Ala Arg Ala Glu Tyr Ser Asn Cys Gly
             20                  25                  30
Glu Asn Glu Tyr Tyr Asn Gln Thr Thr Gly Leu Cys Gln Glu Cys Pro
         35                  40                  45
Pro Cys Gly Pro Gly Glu Glu Pro Tyr Leu Ser Cys Gly Tyr Gly Thr
     50                  55                  60
```

```
Lys Asp Glu Asp Tyr Gly Cys Val Pro Cys Pro Ala Glu Lys Phe Ser
 65                  70                  75                  80
Lys Gly Gly Tyr Gln Ile Cys Arg Arg His Lys Asp Cys Glu Gly Phe
                 85                  90                  95
Phe Arg Ala Thr Val Leu Thr Pro Gly Asp Met Glu Asn Asp Ala Glu
            100                 105                 110
Cys Gly Pro Cys Leu Pro Gly Tyr Tyr Met Leu Glu Asn Arg Pro Arg
        115                 120                 125
Asn Ile Tyr Gly Met Val Cys Tyr Ser Cys Leu Leu Ala Pro Pro Asn
    130                 135                 140
Thr Lys Glu Cys Val Gly Ala Thr Ser Gly Ala Ser Ala Asn Phe Pro
145                 150                 155                 160
Gly Thr Ser Gly Ser Ser Thr Leu Ser Pro Phe Gln His Ala His Lys
                165                 170                 175
Glu Leu Ser Gly Gln Gly His Leu Ala Thr Ala Leu Ile Ile Ala Met
            180                 185                 190
Ser Thr Ile Phe Ile Met Ala Ile Ala Ile Val Leu Ile Ile Met Phe
        195                 200                 205
Tyr Ile Leu Lys Thr Lys Pro Ser Ala Pro Ala Cys Cys Thr Ser His
    210                 215                 220
Pro Gly Lys Ser Val Glu Ala Gln Val Ser Lys Asp Glu Glu Lys Lys
225                 230                 235                 240
Glu Ala Pro Asp Asn Val Val Met Phe Ser Glu Lys Asp Glu Phe Glu
                245                 250                 255
Lys Leu Thr Ala Thr Pro Ala Lys Pro Thr Lys Ser Glu Asn Asp Ala
            260                 265                 270
Ser Ser Glu Asn Glu Gln Leu Leu Ser Arg Ser Val Asp Ser Asp Glu
        275                 280                 285
Glu Pro Ala Pro Asp Lys Gln Gly Ser Pro Glu Leu Cys Leu Leu Ser
    290                 295                 300
Leu Val His Leu Ala Arg Glu Lys Ser Ala Thr Ser Asn Lys Ser Ala
305                 310                 315                 320
Gly Ile Gln Ser Arg Arg Lys Lys Ile Leu Asp Val Tyr Ala Asn Val
                325                 330                 335
Cys Gly Val Val Glu Gly Leu Ser Pro Thr Glu Leu Pro Phe Asp Cys
            340                 345                 350
Leu Glu Lys Thr Ser Arg Met Leu Ser Ser Thr Tyr Asn Ser Glu Lys
        355                 360                 365
Ala Val Val Lys Thr Trp Arg His Leu Ala Glu Ser Phe Gly Leu Lys
    370                 375                 380
Arg Asp Glu Ile Gly Gly Met Thr Asp Gly Met Gln Leu Phe Asp Arg
385                 390                 395                 400
Ile Ser Thr Ala Gly Tyr Ser Ile Pro Glu Leu Leu Thr Lys Leu Val
                405                 410                 415
Gln Ile Glu Arg Leu Asp Ala Val Glu Ser Leu Cys Ala Asp Ile Leu
            420                 425                 430
Glu Trp Ala Gly Val Val Pro Pro Ala Ser Gln Pro His Ala Ala Ser
        435                 440                 445
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<210> 20
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primers used to amplify exon 5 of
EDA1-II.

<400> 20
agaaagcagg acctcctgg 19

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to amplify exon 5 of
EDA1-II.

<400> 21
ctctcaggat cacccactc 19

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to
diagnose ED.

<400> 22
tatgttggct atgactgact gagtgg 26

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to
diagnose ED.

<400> 23
ccctaccaag aaggtagttc 20

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Oligonucleotide primers that can be used to diagnose ED.

<400> 24
ctctcaggat cacccactcc tg 22

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that can be used to diagnose ED.

<400> 25
tgtcaattca ccacagggag 20

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that can be used to diagnos ED.

<400> 26
gaatctagga tgcaggggc 19

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that can be used to diagnose ED.

<400> 27
tattgcggcg aacacg 16

<210> 28
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that can be used to

diagnose ED.

<400> 28
tattgcagcg aacacg 16

<210> 29
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to
diagnose ED.

<400> 29
tattgcggca aaacacg 17

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to screen a BAC
library.

<400> 30
atcatggctg tgcactctag 20

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to screen a BAC
library.

<400> 31
acctactgca tgtctgtgga 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to screen a BAC
library.

<400> 32
cacatgctca gtgttgtcca 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to screen a BAC library.

<400> 33
acacaggctc agtcatgcgg 20

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 34
gcggtgaccc gggagatctg aattc 25

<210> 35
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 35
gaattcagat c 11

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 36
ctgagcggaa ttcgtgagac c 21

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 37
ggtctcacga attccgctca gtt 23

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 38
agtgagaatg atgcctcc 18

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 39
gcctttgttc agtcatagg 19

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 40

cctgagagct ctttgtgag 19

<210> 41
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 41
cgggatcctc gagggggggg ggggggggh 29

<210> 42
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 42
aagcagagct ccacaatc 18

<210> 43
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<220>
<221> misc_feature
<222> (38)..(39)
<223> n represents a, c, t, or g; v represents a, g, or c

<400> 43
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<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 44
ggaacagtca agagcgagtt 20

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers used to clone a murine dl gene.

<400> 45
gcggatccag gccgctctgg acaggatatg 30

<210> 46
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 46
tggtgtctct gatgtgc 17

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 47
acagtggccc ggaagaag 18

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Oligonucleotide primers that were used to clone human DL.

<400> 48
ctgcggtgag aacgagtac 19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that were used to clone human DL.

<400> 49
ggcaaggtgg cgccatgt 18

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that were used to clone human DL.

<400> 50
ggcaccaaag acgaggacta 20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that were used to clone human DL.

<400> 51
tcagcgtcat tctccatgtc 20

<210> 52
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide primers that were used to clone

human DL.

<400> 52
ctagactcga gaattcgcgg ccgcactagt ttttttttt ttttt 46

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 53
tctggtagcc tcctttggaa 20

<210> 54
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 54
ctagactcga gaattcg 17

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 55
tagtcctcgt ctttggtgcc 20

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 56
gagaattcgc ggccgcac 18

<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 57
agccccgtag tctggttgta 20

<210> 58
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 58
gcgtcgacag tgatgagga 19

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 59
cagtcttttg gcaccactca 20

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 60
acgtgtgtgg agtcgtgga 19

<210> 61
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 61
ctcgttggat ccttggctt 19

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 62
tacatgctgg agaacagacc 20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 63
ttccaaagga ggctaccaga 20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 64

ttggcagaag ctcctgaagt 20

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 65
tgctcgagat gtgatgaagg 20

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 66
aagcagatgg ccacagaact 20

<210> 67
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 67
ggagaggatg gcccatgtg 19

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 68
cagaccatgc catagatgtt c 21

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 69
acttcaggag cttctgccaa 20

<210> 70
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 70
tcgtccttgc tcacttggg 19

<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 71
ggatgaattt gagaagctga c 21

<210> 72
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone
human DL.

<400> 72
ctgacttgtt cgtggtggc 19

<210> 73
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that were used to clone human DL.

<400> 73
tccacgactc cacacacgt 19

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for mutation screening of human DL.

<400> 74
aaataaaggt agccagaccc 20

<210> 75
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for mutation screening of human DL.

<400> 75
gtaaggggct cagaccact 19

<210> 76
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for mutation screening of human DL.

<400> 76
catgtgtttc taaggaggta c 21

<210> 77
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 77
caacaatgcc acaagcagga 20

<210> 78
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 78
gtccgtatgg tttggctgc 19

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 79
gccagggttt gccaggag 18

<210> 80
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 80
gtccagctca cctgtctct 19

<210> 81

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 81
accggctctt tcctacacc 19

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 82
tggagcttct ctggatcatt t 21

<210> 83
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 83
aactccaggt gatcgatacc 20

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 84
ctgggtcatt catgccttct 20

<210> 85
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 85
atggtgtgtg gaagccctg 19

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 86
catgagccaa ttctaactcc t 21

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 87
caggacccca gttcagctt 19

<210> 88
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 88
cccaggcact gctaatgac 19

<210> 89
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 89
ccacatctca cagctcatca 20

<210> 90
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 90
tttctactgt tgccccttc t 21

<210> 91
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 91
cccagccctt catgtcagt 19

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 92
tctattgact gtgacttgca 20

<210> 3
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used for
mutation screening of human DL.

<400> 93
ctcgttggat ccttggctt 19

<210> 94
<211> 425
<212> DNA
<213> Homo sapiens

<400> 94
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ggctgaacgt gcccgctcca gcctctccag tgctggaaga gacctctaga tggagcaggt 120
gagtttgcaa ttagggaaag cccctcggca aggactgagt ttccaaactt gcagacaggg 180
cagggagcgg tcaaggaaga gttcccggga agccctttaa acggaaagga agcggggcta 240
gtgtcagaga ggtgtgacag gtcccagtca gccctgctgg cccctaagga catagagtac 300
ctgcttctga gagggctgcc acggtggcca cctgtgaagc ctgtcaccca gaactggatg 360
gtacctgact ttcttcatag acccatcttc tgctgggact gaagctgacc tccaacagaa 420
gccag 425

<210> 95
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(434)
<223> n represents a, c, t, or g

<400> 95
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gtcatgggct gggagagagg ctgggtgcat ttttgaaatg catgtcattt ttgggttgcg 120
tttgaaggtt tcnccaaacc ctctgagcac gagaaacaca atcactancc tcgggtttaa 180
ccttgggccc tccgtgtgct cctagcctcc tntcaggctc cctcccaggc atggctgcna 240
ggctgggaag gccccagagt cagcccaagt ggcatgggtn cagcttcagc ttcatgtctg 300
cttttctttt aggatgtata gtttcccctc tgtttgctgg aaggcacctt atatccagtg 360
gggttaaata aaggtagcca gacccccggc tggggtgcta ccgccagtgc ccagctaatg 420
acgcatnnnt tcag 434

<210> 96
<211> 70
<212> DNA
<213> Homo sapiens

<400> 96
gtgagcccct tgggagagga tggcccatgt gggggactgc acgcagacgc cctggctccc 60
cgtcctggtg 70

<210> 97
<211> 722
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(722)
<223> n is a, c, t or g

<400> 97
gtaagtggtc tgagcccctt acccccacag caccctcatc ctcatgatgg ttggactgtt 60
tcttggcctc ttcagctgta aaatgggaat gctgatcata gtccctcctc cacagggttc 120
ttctgagggt gaaatgaaac caggcctgca aagcacagaa ctctgcccca ggctgaagtt 180
acattgattt cgttggtagc tcccttcata gggtctcatg gatataaacg ttcttgattg 240
cttgtttgtg gtgtgataca cacagccctg tgtctatgtg atgagctcat gcttgggggc 300
cgcgcagcta agaaagactt ggaagactca gacccctacc cccatcctcc tggacacgcc 360
ggtgttctga ggagccactg tattagaggc tcagtggggg acaggggcgc ctcctccatg 420
accttggcaa gtgcgttgat gaggagaact canagcaggc cttgatggtg ggatggggct 480
tggccagcag gggtgaaggc agggtggttc tagtgggggc tggccgtgcc cangtggatc 540
aaccaggagc cactggagac ttaacagcag tgagcactna caagcggcac cttcccagac 600
cgagccccca gcagagcccc caccgcaggg cacccccttc ctatgtcaac cttggggtct 660
tgcaggagtc acatgtgttt ctaaggaggt acggaggcca caacaccccc ctttgttggc 720
ag 722

<210> 98
<211> 123
<212> DNA
<213> Homo sapiens

<400> 98
gtgtctctga tgtgctcagc ccgagcggaa tactcaaact gcggtgagaa cgagtactac 60
aaccagacta cggggctgtg ccaggagtgc cccccgtgtg ggccgggaga ggagccctac 120
ctg 123

<210> 99
<211> 740
<212> DNA
<213> Homo sapiens

<400> 99
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gtcacgctcc ctggacgttg agattgatgg caagagctgc cgtgagccca ggaatggcac 180
tcaccagcta agcattcata aacagatttt tcaggagttc tgaaatgttt ttaaaggatc 240
actttcccac tctaccctga ttaaatgagc gtcagatcat ctgattggaa gcaggattga 300
aatattctcc agtactagta catttttcc tgagtgctgc atctccctcc gcctctgggc 360
aagctaagcc tgagtgttct gttcagcact aagggaaacc tccggggttt cagtgtccgg 420
ttcttgtagc aagctgagga aagtcagatg ccaagtgcta cctgcactgc ctgggcattc 480
cagcagctcg ctgaattcat ctcggggagg ctcagaaaag gggcagcatc tggagcctga 540
gagtggcgag gagaggggca agcccagagc atgagctggt tcctgggggg ttttgcagtt 600
aggacaactc aggaaaccaa ggcccggcaa gagtagcttc tggagacagc tggcacgtca 660
ctgcccaagg actgtgggcc gagtccgtat ggtttggctg ctgcactcac ctgtgtcccc 720
tgtcctcttt ccctggacag 740

<210> 100
<211> 182
<212> DNA
<213> Homo sapiens

<400> 100
tcctgtggct acggcaccaa agacgaggac tacggctgcg tcccctgccc ggcggagaag 60
ttttccaaag gaggctacca gatatgcagg cgtcacaaag actgtgaggg cttcttccgg 120
gccaccgtgc tgacaccagg ggacatggag aatgacgctg agtgtggccc ttgcctccct 180
gg 182

<210> 101
<211> 1169
<212> DNA
<213> Homo sapiens

<400> 101
gtaagcacag gccctcctgg caaaccctgg catgctttct gcagaaaacc ccgaggggct 60
acgggcaagg accttgggaa caggggtcat ggatactgca ggcctcggtg cagccgcaca 120
cctggccttg gtcccatccc acaaggagca gcatccagga cggagagtcc tggcccctcc 180
ggtggacagg cagcccatca ggctctgcct ctgtgtctcc taagtggcca ttaaccatca 240
taatatcttc tgaccaccaa aaggaaacaa attgcttgaa tacttacagt gcagtagccc 300
atgtgaaaca ctttgggaaa aagaaaactn naatttnatg caaaaagcag tattttnagt 360
attctggnaa cactctggnn aanctactaa taannntanat ntgagaaaag aaatatnant 420
gangagatta tgannncgaa gnnaagnnan gnanaancan annaggntnn agaaaatgag 480
gttgnnaang antnataana tagnacanng ntgatatnca tnggaaagta aacngcntga 540
gnannagtga tttgtgatng ccagggtatt cntngaggga aaacangact attggancag 600
anngtgngga aaggnacaaa cgntgtntna ncataganaa nntagagttg ntgggtgggc 660
attnnaanna gcnggtaaag aatagcttgn aagtngncaa ggggtnccag aggcaannnt 720
aatgcctata natcccataa gnntgcaggc tantggngan ggtgctnaca aagagcatgt 780
tcctcctcca ggaaggtctg gccttngttg gtgtnacccc tgggggggcta ancaggccnt 840
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gccaccagag agaggaacca gaaaggggct gagatcaaaa gaaaggccca cgttggcagc 960
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ctgttttgtc cttgtgctct ccnccgtag 1169

<210> 102
<211> 86
<212> DNA
<213> Homo sapiens

<400> 102
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cctggcaccc cccaacacca aggaat 86

<210> 103
<211> 484
<212> DNA
<213> Homo sapiens

<400> 103

gtgagtgtct ttgtccttcc accagcacgg tatttgttca ggcacggatc tctttcacta 60
cagagggtgt aggaaagagc cggtcctggc acctggacaa ggtgaatcac agtaacagca 120
ctagtgaaag tgctcctgtg gcctgtccag gcaggtctat gaagggaggg gcgtttgcca 180
catctgagcc ttgagtcaga ggctgaggtt ctagtgcagg ttggccacca gctacctgac 240
aagtcactta acctccatga gcctcggttt tctcatcggt aatatggggg tgaagaaagn 300
acaatancga tgactcttta gggttcatta aacagtctaa gaaatacaaa tatttagctc 360
ccctcagcca tcactgcctc aggcccattc atgatcatga atccagatcc atgagctctg 420
tggcagcgtg ctttgaaggt ggagcttctc tggatcattt gagggactct attttgcctt 480
gcag 484

<210> 104
<211> 87
<212> DNA
<213> Homo sapiens

<400> 104
gtgtgggagc cacttcagga gcttctgcca acttccctgg cacctcgggc agcagcaccc 60
tgtctccctt ccagcacgcc cacaaag 87

<210> 105
<211> 799
<212> DNA
<213> Homo sapiens

<400> 105
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ctccctaatg taattgaatg acatgttgcc ccccgtgcag gaagtcatta tatctgcaat 180
cagagttgat ccctctatgg gtgtcctggg accgctggga ggtgctggtg gtgaaggcgg 240
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aaccagggaa gangggatcg nggaggaccc caangtttan tntgcctctc acanttagnc 480
ccccacntgg cttgncntna aggttgccaa agcagtagna gcgagaagca agctccctta 540
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gggttgtggg cagtcctggt ctggcagcca aaaccagcgc gnaggatttg gttctcagtc 660
taagcaagca cctcagattt cagggttccc tgaaagcatc ccaggggcag ggccattgct 720
tccaggggcc ggagtcctgg agggaagacc agcagggatc ctgagctctg ggtcattcat 780
gccttctctc cacccacag 799

<210> 106
<211> 126
<212> DNA
<213> Homo sapiens

<400> 106
aactctcagg ccaaggacac ctggccactg ccctgatcat tgcaatgtcc accatcttca 60
tcatggccat cgccatcgtc ctcatcatca tgttctacat cctgaagaca aagccctctg 120
ccccag 126

<210> 107
<211> 96
<212> DNA

<213> Homo sapiens

<400> 107
gtgacggccc ccatgcgccg gtgccctgcc tcctggactc tccgtcaact ccccctgtcg 60
gagagcctgg ctgctcactc cctcctctct ccccag 96

<210> 108
<211> 75
<212> DNA
<213> Homo sapiens

<400> 108
cctgttgcac cagccacccg gggaagagcg tggaggccca agtgagcaag gacgaggaga 60
agaaagaggc cccag 75

<210> 109
<211> 243
<212> DNA
<213> Homo sapiens

<400> 109
gtctgtgaac cagggcttcc acacaccatg tgcacggtgc ccatctctgg gtggagggcg 60
ttcccagaag cagcctcctc gctgcttctg ctctcacatg ctgaaccata ctgtgcttac 120
cgtggggtgg tgccacacag acaccgggca gctctgccca acaggaagag cagggttggg 180
ctgagcgcan agccatgagc caattctaac tcctatctcc ccaacctccc catttccctg 240
cag 243

<210> 110
<211> 73
<212> DNA
<213> Homo sapiens

<400> 110
acaacgtggt gatgttctcc gagaaggatg aatttgagaa gctgacagca acttcagcaa 60
agcccaccaa gag 73

<210> 111
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 111
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ccagcccang agcaaggtgc ttggaatcat ccctggttat aggaatacca cactgaggta 540
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gcactgctaa tgaccatcgc tcttgttttt gcag 1174

<210> 112
<211> 160
<212> DNA
<213> Homo sapiens

<400> 112
cgagaacgat gcctcatcng agaatgagca gctgctgagc cggagcgtcg acagtgatga 60
ggagcccgcc cctgacaagc agggctcccc ggagctgtgc ctgctgtcgc tggttcacct 120
ggccagggag aagtctgcca ccagcaacaa gtcagccggg 160

<210> 113
<211> 226
<212> DNA
<213> Homo sapiens

<400> 113
gtgaggctcc tgcaggtgcc atgatgagct gtgagatgtg gctccctcac agccgcaagg 60
actaaaactt tcttattgaa tcagctctcc tgcaagacgg ggtgtttctc ccagaagtcc 120
aagataggag acctggacag tgacaagttc acagcaagat agtcaaaagg gaaaaaaacc 180
ctttcgtttt tgagttttgt ttttttttn ggngatgana gnctng 226

<210> 114
<211> 61
<212> DNA
<213> Homo sapiens

<400> 114
attcaaagcc ggaggaaaaa gatcctcgat gtgtatgcca acgtgtgtgg agtcgtggaa 60
g 61

<210> 115
<211> 309
<212> DNA
<213> Homo sapiens

<400> 115
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agnagtgaga ngggaaggna nagngagnag gggnnangag aaagngggag ngtaggnggc 180
gatgngnnng gtngaaatat tnanagaaat tttttcaaat aatttttatt tcatttaaat 240
aatttttcag tgttgacctt ctattgactg tgacttgcaa catctaactg tggccattgg 300
tgtctgtag 309

<210> 116
<211> 2781
<212> DNA
<213> Homo sapiens

<400> 116
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gcacggcagg ctacagcatc cctgagctac tcacaaaact ggtgcagatt gagcggctgg 240
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aaaaaaaaaa aaaaaaaaaa a 2781

<210> 117

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to diagnosis ED.

<400> 117
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<210> 118
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers that can be used to diagnosis ED.

<400> 118
agaaagcagg acctcctgg 19

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify TNF homology domain of mouse dl.

<400> 119
ggattccagg aacaactgtt atgg 24

<210> 120
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify TNF homology domain of mouse dl.

<400> 120
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<210> 121
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify
TNF homology domain of mouse dl.

<400> 121
gtcgacgaaa atcagccagc tg 22

<210> 122
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primer that can be used to amplify
TNF homology domain of mouse dl.

<400> 122
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